

domain-containing human slap homologue having immune cell-specific
expression
Patent: WO 0242457-A 1 30-MAY-2002;
Bristol-Myers Squibb Co. (US)

FEATURES
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/organism="Homo sapiens"
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Query Match 100.0%; Score 2567; DB 6; Length 2567;
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Matches 2567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Kawabata, A., Hiki, T., Kobayashi, N., Inagaki, H., Ikema, Y.,
 Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
 Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 JOURNAL 2 (bases 1 to 2415)
 AUTHORS Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
 Shibahara, T., Tanaka, T. and Nakamura, Y.
 TITLE Direct Submission 2 g/h
 JOURNAL Submitted (29-AUG-2000) Sumitomo Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure Analysis, Human
 Genome Center, Shirokane-da, 4-6-1, Minato-ku, Tokyo 108-8639,
 Japan (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 Fax:81-3-5449-5416)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing; Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing; Department of

Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).

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 VERSION AX443135.1 GI:21690556
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 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Burgess, C.E., Conley, P.B., Grosse, W.M., Hart, M., Kekuda, R.,
 Shimkets, R.A., Spytek, K.A., Szekeres, E.S., Tomlinson, J.E.,
 Topper, J.N. and Yang, R.B.
 Proteins and nucleic acids encoding same
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BASE COUNT 240 a 333 c 359 g 251 t
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 Best Local Similarity 99.9%; Pred. No. 0;
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Qy 18 AGCTAGAGCTCCCAAGGAGACCCACGCTGTGTCTGTGAGACAGAGCTCAAGGAGCCCTGGG 77
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Qy 78 CTTTCCCTCCCTGGCTGGCTGTGTGTGGAGGGTCCCAAGTCCCAAGATCCCTTAAGAG 137
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TITLE
JOURNAL
COMMENT

Grand-Pierre, N., Gilev, I., Johnson, R., Jones, C., Kamm, L., Kartas, A.,
 Howland, J.C., Miller, J., Naylor, T., Norman, C.H., O'Connor, I., O'Donnell, P.,
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 Roy, A., Santos, R., Schaner, S., Severy, P., Spencer, B.,
 Stange, Thomas, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Stejave, S., Theodorou, J., Tirrell, A., Travers, M., Trigilio, J.,
 Vassilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J.
 Young, G., Zainoun, K., Zimmer, A. and Zody, M.
 Direct Submissions
 Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genomes
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 27, 2000 this sequence version replaced g1:7283243.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996) 1997
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information
 Center project name: L7115
 Center clone name: 712.N.14

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 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.96.07.11
 Consensus quality: 125577 bases at least Q40
 Consensus quality: 135703 bases at least Q30
 Consensus quality: 139593 bases at least Q20
 Insert size: 182000; agarose-fp
 Insert size: 14223; sum-of-coverage
 Quality coverage: 2.6 in Q20 bases; sum-of-coverage
 Quality coverage: 3.3 in Q20 bases; sum-of-coverage

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 37 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1214: contig of 1214 bp in length
 * 1215 1314: gap of 100 bp
 * 1315 2673: contig of 1359 bp in length
 * 2674 2773: gap of 100 bp
 * 2774 4520: contig of 1747 bp in length
 * 4521 4620: gap of 100 bp
 * 4621 5961: contig of 1341 bp in length
 * 5962 6061: gap of 100 bp
 * 6062 7719: contig of 1658 bp in length
 * 7720 7819: gap of 100 bp
 * 7820 9793: contig of 1980 bp in length
 * 9800 9899: gap of 100 bp
 * 9900 11434: contig of 1535 bp in length
 * 11435 11534: gap of 100 bp
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Grand-pré, N., Grant, G., Hagos, R., Heaford, A., Hottel, L.,
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 Young, G., Zannou, J., Zimmer, A. and Zody, W.
 Direct Submission
 Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research,
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr. 27, 2000 this sequence version replaced g1:7283243.
 All repeats were identified using RepeatMasker:
 Smt, A. P. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/MW/RepeatMasker.html

 Project Information
 Center: Whitehead Institute/ MIT Center for Genome Research
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu

 Project Information
 Center project name: L7115
 Center clone name: 712.N.14

 Summary Statistics
 Sequencing vector: M13, M7815, 100% of reads
 Chemistry: Dye-terminator Big Dye, 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 125677 bases at least Q40
 Consensus quality: 135703 bases at least Q30
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 Insert size: 182000, agarose-fp
 Insert size: 122233, sum-of-contigs
 Quality coverage: 2.6 in Q20 bases; agarose-fp
 Quality coverage: 3.3 in Q20 bases; sum-of-contigs

 NOTE: This is a 'working draft' sequence. It currently
 consists of 37 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.
 1 1214: contig of 1214 bp in length
 1215 1314: gap of 100 bp
 1315 2673: contig of 1359 bp in length
 2674 2773: gap of 100 bp
 2774 4520: contig of 1747 bp in length
 4521 4620: gap of 100 bp
 4621 5961: contig of 1341 bp in length
 5962 6061: gap of 100 bp
 6062 7719: contig of 1658 bp in length
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 9800 9899: gap of 100 bp
 9900 11433: contig of 1535 bp in length
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VERSION AF326353.1 GI:17351920
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Loreto, M.P. and McGlade, C.J.
TITLE Direct Submision
JOURNAL Submitted (28-JUL-2000) Brain Tumour Research Centre, Hospital for
Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada
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ACCESSION AF326353
VERSION AF326353.1 GI:16797891
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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1 (bases 1 to 786)
AUTHORS Holland, S.J., Liao, X.C., Mendenhall, M.K., Zhou, X., Pardo, J.,
Shen, M., Yu, S., Chan, E., Fu, A.C., Sheng, N., Yu, P., Pali, E., Nagin, A.,
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Payan, D.G., Manobo, H.S.Y. and Wu, U.
TITLE Functional Cloning of Src-like Adaptor Protein-2 (SLAP-2), a Novel
Inhibitor of Antigen Receptor Signaling
JOURNAL J. Exp. Med. 194 (9), 1263-1276 (2001)

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MEDLINE 21553259
PUBMED 11695982
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AUTHORS Holland,S.J., Mendenhall,M.K., Zhou,X., Spencer,C., Pardo,J.,
Fu,A.C., Sheng,N., Shen,M., Liao,C., Luo,Y., Payan,D.G.,
Manebo,H.S.Y. and Wu,J.
TITLE Direct Submission
JOURNAL Submitted (05-DEC-2000) Rigol Pharmaceutical Inc., 240 East Grand
Avenue, South San Francisco, CA 94080, USA
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Best Local Similarity 100.0%; Pred. No. 1.9e-217;
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 541 GATGACATCTGCTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
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Db 781 GCCTAG 786
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LOCUS Homo sapiens Src-like adaptor protein-2 splice isoform mRNA,
DEFINITION complete cds.
ACCESSION AF290986
VERSION AF290986.1 GI:17351922
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 737)
AUTHORS Loreto,M.P. and McGlade,C.J.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-2000) Brain Tumour Research Centre, Hospital for
Sick Children, 555 University Avenue, Toronto, Ont M5G 1X8, Canada
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Best Local Similarity 93.4%; Pred. No. 9.8e-182;
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QY 535 GGCAGTTTCCCGCAGGTGGCCCGGCGGAGCTGCTGCTGAGAGAGAGAGAGAGAGAGAG 594
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QY 595 ATGCTCTCTGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATG 654
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RESULT 10
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 ACCESSION AF434990.1 GI:19224130
 VERSION
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 SOURCES
 ORGANISM
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1321)
 Pandey,A., Ibarrola,N., Kratchmarova,I., Fernandez,M.M.,
 Constantinescu,S.N., Ohara,O., Sawadhihoel,S., Lodish,H.F. and
 Mann,M.
 A novel Src homology 2 domain-containing molecule, Src-like adapter
 protein-2 (SLAP-2), which negatively regulates T cell receptor
 signaling
 J. Biol. Chem. 277 (21), 19131-19138 (2002)
 MEDLINE 22013997
 PUBMED 11891219
 REFERENCE 2 (bases 1 to 1321)
 AUTHORS Ibarrola,N., Mann,M. and Pandey,A.
 TITLE Direct Submission
 JOURNAL Submitted (16-OCT-2001) Whitehead Institute for Biomedical
 Research, Nine Cambridge Center, Cambridge, MA 02142, USA
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 Qy 411 AACATGGGAAGTCTGCGCAGAGAGAAATCTGCGCAAGCCCAAGCTTGAATTCCTC 470
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Qy 189 TCGTAGGCTACCCAAACCAACACCTAGCTCTCCCTGAGAGATCTCCAGGCTGAGAGAG 248
Db 11769 TCGTAGGCTACCCAAACCAACACCTAGCTCTCCCTGAGAGATCTCCAGGCTGAGAGAG 11710
Qy 249 TTCTGGGTCTCTTGAACCAAGACATCTGGGACACTTCCAGAGGGCCCCCAAGCCCTTA 308
Db 11709 TTCTGGGTCTCTTGAACCAAGACATCTGGGACACTTCCAGAGGGCCCCCAAGCCCTTA 11650

Qy 309 ACCTGTCAGCAGCAGATGCTCTTCAGCAGAGCTGTTCCCAAGCTTTGATGACAA 368
Db 11649 ACCTGTCAGCAGCAGATGCTCTTCAGCAGAGCTGTTCCCAAGCTTTGATGACAA 11590
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RESULT 13
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LOCUS Homo sapiens chromosome 20 clone RP11-712N14 map 20, WORKING DRAFT
DEFINITION SEQUENCE 37 unordered pieces.
ACCESSION AC026539
VERSION AC026539.2 GI:7656813
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eumetazoa; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bede, F., Boguslavsky, L., Bouckgele, B., Brown, A., Burkett, G., Campiani, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S., Colymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Galdyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hages, B., Heatford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Laroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McGowan, P., McGurk, A., McKernan, K., McPherson, R., Meidard, J., Menus, L., Mihova, T., Miranda, C., Mienga, V., Morion, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talmas, J., Teefaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT
Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 27, 2000 this sequence version replaced gi:7283243.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L7115
Center clone name: 712 N 14
----- Summary Statistics
Sequencing vector: M13, M7815, 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 125577 bases at least Q40
Consensus quality: 135703 bases at least Q30
Consensus quality: 139593 bases at least Q20
Insert size: 18200; agarose-fp
Insert size: 18200; sum-of-ctg
Quality coverage: 2.6 in Q20 bases; agarose-fp

Quality coverage: 3.3 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1315 2673: contig of 1359 bp in length
2674 2773: gap of 100 bp
2774 4520: contig of 1747 bp in length
4521 4620: gap of 100 bp
4621 5961: contig of 1341 bp in length
5962 6061: gap of 100 bp
6062 7719: contig of 1658 bp in length
7720 9759: contig of 1980 bp in length
9800 9899: gap of 100 bp
9900 11434: contig of 1535 bp in length
11435 11534: gap of 100 bp
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FEATURES

source

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Matches 371; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Best Local Similarity 80.2%; Pred. No. 2.3e-61;
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Db 8478 GACAGGTTTACCATTTGCGCAGGCTGTGTGAATCTCTGACCTGAGTATCCACC 8537
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Oy 2138 TCAGATCT 2145
Db 8598 TACCACT 8605

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RESULT 15
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DEFINITION Homo sapiens chromosome 1 Clone RP11-145H3, complete sequence.
ACCESSION AC099066 AL559830
VERSION AC099066.2 GI:18958741
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
REFERENCE Submitted (08-NOV-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
JOURNAL 3 (bases 1 to 149548)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Feb 27, 2002 this sequence version replaced gi:16799024.
COMMENT ----- Genome Center
Center: University of Washington Genome Center
Center Code: UWGC
Web site: http://www.genome.washington.edu
Contact: uwgchgs@u.washington.edu
Drafting Center: SC
----- Project Information
Center project name: chr-1
Center clone name: RP11-145A3 (ac0642)
----- Summary Statistics
Sequencing vector: plasmid; 44% of reads
Chemistry: Dye-terminator ET; 68% of reads
Chemistry: Dye-terminator Big Dye; 32% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149371 bases at least Q40
Consensus quality: 149548 bases at least Q40
Insert size: 40578; sum-of-contigs
Quality coverage: 28.0x in Q20 bases; sum-of-contigs

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Overlapping Sequences:
5': Mapping in progress
3': RP11-92N17 AL513528

Sequence Quality Assessment:
This entry has been annotated with sequence quality

estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest
fingerprinting. Comparison of the experimentally derived digest
fragments with sequence-predicted fragments is given below.
The electronically-digested sequence consists of both insert and
vector, in order to accurately represent the entire circular BAC.
Small fragments below a variable cutoff (approximately 400-800 bp)
are not resolved in the fingerprint and hence do not appear
in the table. There are no significant remaining discrepancies
between the experimental and predicted values. Uniquely ordered
fragments are separated by dashed lines.

BglIII

ECORI

HandIII

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7096	7367	677	<800	5513	5510
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FEATURES

source

misc_feature

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Tue Apr 1 06:01:19 2003

us-09-988-971-1.rge

Page 20

ATCATGCCGCGAGATGCCGCTGCTTGAGCGAALACTGCTGTAACGCCATCGAAAC

Query Match	Score	DB	Length
9.8%	251.2	9	149548

Best Local Similarity 80.2%; Pred: No. 2.3e-61;
Matches 295; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Matches 295; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1778 CTGGGAGACTCTAGGCTCTCAAAATGTCCTCCCATTTGAGAGCAAAAGCCCACTCTTTT 1837
Db 65460 CTCGAGTAGTCCCTCTAGTGTAGTGTCTTTCTTTAGAAAGAGTAACTCTATCTT 65401
QY 1838 CTTTTTTTTGAGACGAGTCTTGCCCTCTTCTCCATCTGGAGTCMAATGGCAAGATC 1897
Db 65400 TTTTTTTTTGAAATGAGTCTCTCTGTGGTCCGAGGCTGAGTGAATGGGCAATCT 65341
QY 1898 CAGCTCACTGCAACTCATCTCTGATTCAAACAATTCTCTGCTCTAGCCTCAGAA 1957
Db 65340 CGGCTCACTGCAACTCTGCTCTCTGGATTCAACATTTCTCTGCTCTAGCCTCCAG 65281
QY 1958 TAGCTGGGATTAAAGGCGTAAACACACATGGCTGGCAATTTTTTGATTTTAGTA 2017
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